

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 20:05:04 ; Search time 2.79577 Seconds
(without alignments)
8779.016 Million cell updates/sec

Title: US-10-750-976-38

Perfect score: 15

Sequence: 1 ctgacctagggcgca 15

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues 2405568

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA:
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2: /cgn2_6/ptodata/1/ina/5B COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 93.3 | 1353 | 3 | US-09-134-001C-1974 | Sequence 1974, Ap |
| 4 | 93.3 | 3017 | 4 | US-09-710-279-4422 | Sequence 4422, Ap |
| 5 | 93.3 | 3233 | 4 | US-09-710-279-3586 | Sequence 3586, Ap |
| 6 | 93.3 | 4185 | 4 | US-09-710-279-3646 | Sequence 3646, Ap |
| 7 | 89.3 | 601 | 4 | US-09-949-016-157837 | Sequence 157837, Ap |
| 8 | 89.3 | 1884 | 4 | US-09-902-540-8567 | Sequence 8567, Ap |
| 9 | 89.3 | 11382 | 4 | US-09-902-540-904 | Sequence 904, App |
| 10 | 89.3 | 79756 | 4 | US-09-949-016-17537 | Sequence 17537, A |
| 11 | 89.3 | 191433 | 4 | US-09-949-016-16144 | Sequence 16144, A |
| 12 | 86.7 | 601 | 4 | US-09-949-016-132415 | Sequence 132415, A |
| 13 | 86.7 | 601 | 4 | US-09-949-016-161664 | Sequence 161664, A |
| 14 | 86.7 | 8264 | 4 | US-09-949-016-203414 | Sequence 203414, A |
| 15 | 86.7 | 54531 | 4 | US-09-949-016-15457 | Sequence 15457, A |
| 16 | 86.7 | 76962 | 4 | US-09-949-016-16267 | Sequence 16267, A |
| 17 | 86.7 | 325791 | 4 | US-09-949-016-17482 | Sequence 17482, A |
| 18 | 86.7 | 450395 | 4 | US-09-768-185A-1 | Sequence 1, Appl1 |
| 19 | 86.7 | 670689 | 4 | US-09-949-016-15473 | Sequence 15473, A |
| 20 | 86.7 | 670689 | 4 | US-09-949-016-12505 | Sequence 12505, A |
| 21 | 86.7 | 670689 | 4 | US-09-949-016-14207 | Sequence 14207, A |
| 22 | 86.7 | 4403765 | 3 | US-09-103-840A-2 | Sequence 2, Appl1 |
| 23 | 86.7 | 4411529 | 3 | US-09-103-840A-1 | Sequence 1, Appl1 |
| 24 | 82.7 | 25 | 4 | US-09-386-196G-117504 | Sequence 117504, A |
| 25 | 82.7 | 25 | 4 | US-09-386-196G-117515 | Sequence 117515, A |
| 26 | 82.7 | 25 | 4 | US-09-386-196G-117517 | Sequence 117517, A |
| 27 | 82.7 | 258 | 4 | US-09-107-532A-428 | Sequence 428, App |

ALIGNMENTS

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| 28 | 12.4 | 82.7 | 265 | 4 | US-09-513-999C-10978 | Sequence 10978, A |
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| 30 | 12.4 | 82.7 | 434 | 4 | US-09-270-767-4883 | Sequence 4883, Ap |
| 31 | 12.4 | 82.7 | 434 | 4 | US-09-270-767-20165 | Sequence 20165, A |
| 32 | 12.4 | 82.7 | 525 | 4 | US-09-252-991A-2828 | Sequence 2828, Ap |
| 33 | 12.4 | 82.7 | 540 | 2 | US-08-448-561-3 | Sequence 3, Appl1 |
| 34 | 12.4 | 82.7 | 774 | 4 | US-09-270-767-2784 | Sequence 2784, Ap |
| 35 | 12.4 | 82.7 | 774 | 4 | US-09-270-767-18066 | Sequence 18066, A |
| 36 | 12.4 | 82.7 | 1272 | 4 | US-09-328-352-560 | Sequence 560, App |
| 37 | 12.4 | 82.7 | 1659 | 4 | US-09-252-991A-9018 | Sequence 9018, Ap |
| 38 | 12.4 | 82.7 | 2031 | 2 | US-08-448-561-2 | Sequence 2, Appl1 |
| 39 | 12.4 | 82.7 | 2310 | 4 | US-09-252-991A-3040 | Sequence 3040, Ap |
| 40 | 12.4 | 82.7 | 7374 | 4 | US-09-252-991A-9100 | Sequence 9100, Ap |
| 41 | 12.4 | 82.7 | 7518 | 4 | US-09-620-312D-1051 | Sequence 1051, Ap |
| 42 | 12.4 | 82.7 | 8931 | 3 | US-09-051-019-1 | Sequence 1, Appl1 |
| 43 | 12.4 | 82.7 | 15472 | 3 | US-09-453-702B-71 | Sequence 71, Appl1 |
| 44 | 12.4 | 82.7 | 49389 | 4 | US-09-949-016-12547 | Sequence 12547, A |
| 45 | 12.4 | 82.7 | 49389 | 4 | US-09-949-016-13630 | Sequence 13630, A |

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RESULT 1
US-09-204-117B-5
; Sequence 5, Application US/09204117B
; Patent No. 6413768
; GENERAL INFORMATION:
; APPLICANT: Galen, James
; TITLE OF INVENTION: PLASMID MAINTENANCE SYSTEM FOR ANTIGEN DELIVERY
; FILE REFERENCE: 4135-101
; CURRENT APPLICATION NUMBER: US/09/204,117B
; CURRENT FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: mutated Shiga toxin segment
US-09-204-117B-5

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Best Local Similarity 100.0%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACCTAGGGCGCA 15
Db 1 CTGACCTAGGGCGCA 15

RESULT 2
US-09-710-279-1473
; Sequence 1473, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1473
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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OM nucleic - nucleic search, using sw model

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(without alignments)
10487.183 Million cell updates/sec

Title: US-10-750-976-37

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Scoring table: IDENTITY NUC
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Total number of hits satisfying chosen parameters: 9416466

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 93.3 | 714 | 9 | HS4327219 | HS4327219 Homo sapi |
| 4 | 93.3 | 3312 | 3 | AY433803 | AY433803 Trypanoso |
| 5 | 93.3 | 5069 | 5 | AF038560 | AF038560 Gallus ga |
| 6 | 93.3 | 10221 | 1 | AE014558 | AE014558 Brucella |
| 7 | 93.3 | 10495 | 1 | AE009700 | AE009700 Brucella |
| 8 | 93.3 | 24523 | 1 | AE008756 | AE008756 Salmone |
| 9 | 93.3 | 36748 | 7 | AY539836 | AY539836 Burkholde |
| 10 | 93.3 | 39949 | 3 | AC009782 | AC009782 Leishman |
| 11 | 93.3 | 106256 | 3 | AC108135 | AC108135 Leishman |
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| 13 | 93.3 | 133713 | 3 | AC087838 | AC087838 Leishman |
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| 15 | 93.3 | 152770 | 9 | AC013602 | AC013602 Homo sapi |
| 16 | 93.3 | 173839 | 9 | AC026005 | AC026005 Homo sapi |
| 17 | 93.3 | 181097 | 2 | AC118205 | AC118205 Mus muscu |
| 18 | 93.3 | 217285 | 2 | AC126317 | AC126317 Rattus no |
| 19 | 93.3 | 233050 | 1 | AL627271 | AL627271 Salmone |

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| C 20 | 14 | 93.3 | 260760 | 2 | AC127861 | AC127861 Rattus no |
| C 21 | 14 | 93.3 | 295050 | 1 | AL591982 | AL591982 Listeria |
| C 22 | 14 | 93.3 | 300523 | 1 | AE016838 | AE016838 Salmone |
| C 23 | 14 | 93.3 | 305325 | 1 | AE016765 | AE016765 Escherich |
| C 24 | 14 | 93.3 | 311600 | 1 | AE016871 | AE016871 Pseudomon |
| C 25 | 14 | 93.3 | 340750 | 1 | EX294135 | EX294135 Pirellula |
| C 26 | 14 | 93.3 | 349980 | 6 | AK641671 | AK641671 Sequence |
| C 27 | 13.4 | 89.3 | 155 | 8 | HV19R | HV19R Sequence |
| C 28 | 13.4 | 89.3 | 227 | 8 | HVE1323LR | HVE1323LR Sequence |
| C 29 | 13.4 | 89.3 | 231 | 8 | HVE1329TR | HVE1329TR Sequence |
| C 30 | 13.4 | 89.3 | 232 | 8 | HVE1324MR | HVE1324MR Sequence |
| C 31 | 13.4 | 89.3 | 243 | 6 | AR321328 | AR321328 Sequence |
| C 32 | 13.4 | 89.3 | 318 | 6 | AX048488 | AX048488 Sequence |
| C 33 | 13.4 | 89.3 | 318 | 6 | AX048489 | AX048489 Sequence |
| C 34 | 13.4 | 89.3 | 356 | 8 | HVE08492R | HVE08492R Sequence |
| C 35 | 13.4 | 89.3 | 413 | 6 | CO481384 | CO481384 Sequence |
| C 36 | 13.4 | 89.3 | 640 | 14 | AF322856 | AF322856 Caprine a |
| C 37 | 13.4 | 89.3 | 798 | 6 | AR388811 | AR388811 Sequence |
| C 38 | 13.4 | 89.3 | 817 | 8 | PSU58023 | PSU58023 Pseudorogsn |
| C 39 | 13.4 | 89.3 | 858 | 11 | CNS0603B | CNS0603B Sequence |
| C 40 | 13.4 | 89.3 | 1074 | 6 | AR386605 | AR386605 Sequence |
| C 41 | 13.4 | 89.3 | 1104 | 8 | AB189674 | AB189674 Philodend |
| C 42 | 13.4 | 89.3 | 1238 | 1 | AB174823 | AB174823 Cellulomo |
| C 43 | 13.4 | 89.3 | 1281 | 9 | BC064028 | BC064028 Homo sapi |
| C 44 | 13.4 | 89.3 | 1404 | 3 | AF026516 | AF026516 Funiculin |
| C 45 | 13.4 | 89.3 | 1539 | 6 | AX568254 | AX568254 Sequence |

ALIGNMENTS

| | | | | | |
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| RESULT 1 | AY547458 | 3959 bp | RNA | linear | VRL 04-AUG-2004 |
| LOCUS | AY547458 | | | | |
| DEFINITION | Avian orthoreovirus inner capsid protein lambda-A gene, complete cds. | | | | |
| ACCESSION | AY547458 | | | | |
| VERSION | AY547458.1 | GI:47420812 | | | |
| KEYWORDS | Avian orthoreovirus | | | | |
| SOURCE | Avian orthoreovirus | | | | |
| ORGANISM | Virus; dsRNA viruses; Reoviridae; Orthoreovirus. | | | | |
| REFERENCE | 1. (bases 1 to 3959) | | | | |
| AUTHORS | Touris-Otero, F., Cortez-San Martin, M., Martinez-Coostas, J. and Benavente, J. | | | | |
| TITLE | Avian Reovirus Morphogenesis Occurs Within Viral Factories and Begins with the Selective Recruitment of sigmans and lambda to muns Inclusions | | | | |
| JOURNAL | J. Mol. Biol. 341 (2), 361-374 (2004) | | | | |
| PUBMED | 15276829 | | | | |
| REFERENCE | 2. (bases 1 to 3959) | | | | |
| AUTHORS | Cortez-San Martin, M., Touris-Otero, F., Martinez-Coostas, J. and Benavente, J. | | | | |
| TITLE | Direct Submision | | | | |
| JOURNAL | Submitted (13-FEB-2004) Bioguinica, Universidad de Santiago de Compostela, Facultad de Farmacia Campus Sur s/n, Santiago de Compostela, La Coruna 15782, Spain | | | | |
| FEATURES | Location/Qualifiers | | | | |
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| | /translation="MSSRRVARRRKKDTSKDTKTKSKRSSTDAKSTSDADKX VTAAPPNNPAATPSSTDCASGTSYAKQTHDASVKSAPRTYSSGCKDSMRGAVK SODAKATVAVDNNKRDVDFGAGSGDKNAITKTSVNDGKRVPAKADATISSAKA | | | | |

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 16:32:44 / Search time 20.7192 Seconds
(without alignments)
9714.213 Million cell updates/sec

Title: US-10-750-976-36

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Scoring table: IDENTITY NUC
Gapop 10'-0, Gapext 1.0

Searched: 4390206 seqs, 2359870667 residues

Total number of hits satisfying chosen parameters: 8780412

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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6: geneseq20038.*
7: geneseq20048.*
8: geneseq20058.*
9: geneseq20068.*
10: geneseq20078.*
11: geneseq20088.*
12: geneseq20098.*
13: geneseq20108.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 26 | 76.5 | 33 | 3 | AAA07572 Modified |
| 2 | 26 | 76.5 | 4196 | 3 | AAA0825 Expressio |
| 3 | 23 | 67.6 | 32 | 3 | AAA07567 Modified |
| 4 | 22.8 | 67.1 | 59 | 3 | AAA0809 PCR prime |
| 5 | 22.2 | 65.3 | 349 | 5 | ABV09570 Human pro |
| 6 | 22.2 | 65.3 | 400 | 5 | ABV0746 Human pro |
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| 18 | 19.8 | 58.2 | 82938 | 6 | ABV2623 Murine tra |
| 19 | 19.8 | 58.2 | 110000 | 13 | ABV2623 Murine tra |
| 20 | 19.8 | 58.2 | 167739 | 9 | AAV58258 Murine tu |

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| 21 | 19.6 | 57.6 | 414 | 10 | ADBS9176 Rat gene |
| 22 | 19.6 | 57.6 | 650 | 3 | AAV51918 Arabidops |
| 23 | 19.6 | 57.6 | 782 | 3 | AAV51918 Arabidops |
| 24 | 19.6 | 57.6 | 879 | 6 | ABV21388 Arabidops |
| 25 | 19.6 | 57.6 | 1051 | 6 | ABV21388 Arabidops |
| 26 | 19.6 | 57.6 | 1140 | 3 | AAV51918 Arabidops |
| 27 | 19.6 | 57.6 | 1189 | 3 | AAV51918 Arabidops |
| 28 | 19.4 | 57.1 | 1907 | 4 | AAV51918 Arabidops |
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| 33 | 19.4 | 57.1 | 2152 | 4 | AAV51918 Arabidops |
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| 36 | 18.8 | 55.3 | 1497 | 10 | ADBS1378 Arabidops |
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| 38 | 18.8 | 55.3 | 1764 | 10 | ADBS1378 Arabidops |
| 39 | 18.8 | 55.3 | 28903 | 11 | ACN44636 Mouse gen |
| 40 | 18.8 | 55.3 | 32249 | 4 | AAV51918 Arabidops |
| 41 | 18.8 | 55.3 | 32249 | 4 | AAV51918 Arabidops |
| 42 | 18.8 | 55.3 | 170834 | 10 | ADBS1378 Arabidops |
| 43 | 18.8 | 55.3 | 192427 | 10 | ADBS1378 Arabidops |
| 44 | 18.8 | 55.3 | 214019 | 10 | ADBS1378 Arabidops |
| 45 | 18.8 | 55.3 | 319608 | 3 | AAV51601 Human chr |

ALIGNMENTS

| | |
|----------|---|
| RESULT 1 | AAA07572 standard; DNA; 33 BP. |
| ID | AAA07572 |
| XX | AAA07572: 29-AUG-2000 (first entry) |
| XX | DE Modified ompc promoter. |
| XX | Expression cassette; plasmid maintenance system; Neisseria meningitidis; |
| XX | post-segregational killing function; ompc promoter; immune response; |
| XX | KW vaccine; Salmonella typhi; hepatitis; Haemophilus influenzae type b; |
| XX | acellular pertussis; varicella; rotavirus; Streptococcus pneumoniae; |
| XX | KW cancer vaccine; autoimmune disorder; immunological disease; allergy; |
| XX | myasthenia gravis; lupus erythematosus; rheumatoid arthritis; therapy; |
| XX | multiple sclerosis; asthma; ss. |
| XX | Unidentified. |
| XX | OS |
| XX | PN WO200032047-A1. |
| XX | PD 08-JUN-2000. |
| XX | PF 02-DEC-1999; 99WO-US028499. |
| XX | PR 02-DEC-1998; 98US-00204117. |
| XX | PR 12-OCT-1999; 99US-0158738P. |
| XX | (UYMA-) UNIV MARYLAND BALTIMORE. |
| XX | Galen UE; |
| XX | WPI; 2000-412091/35. |
| XX | Expression cassette used as live vector vaccine comprises nucleotide |
| XX | sequence encoding origin of replication and plasmid maintenance system |
| XX | which includes a post-segregational killing and a partitioning function. |
| XX | Claim 145; Page 102; 127P; English. |
| XX | This sequence represents a modified ompc promoter, and can be used in the |
| XX | expression cassette of the invention. The cassette is an independently |

| | Query Match | 100.0% | Score 4196; | DB 6; | Length 4196; |
|----|-----------------------|---|---------------|-----------|--------------|
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| Db | 61 | GCGAGGATCCGGTTGAAATATAGGGGTAAACAGACATTCAGAAATGATGACGGTAAATAAA | 120 | | |
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| QY | 241 | GAGTTAGAGTGCTATTTGGCCATTCGCGAAATAATCTTAAAAAGTCCCTTGCAATTACA | 300 | | |

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 11:14:05 / Search time 83.643 Seconds
(without alignments)
8669.645 Million cell updates/sec

Title: US-10-750-965-39
Perfect score: 15
Sequence: 1 gaattcgagaccagt 15

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 5 | 15 | 100.0 | 190107 | 2 AC100832 | AC100832 Homo sapi |
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| C 25 | 14 | 93.3 | 1681 | 9 AK000455 | AK000455 Homo sapi |
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| C 28 | 14 | 93.3 | 2133 | 6 AK027380 | AK027380 Homo sapi |
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| C 30 | 14 | 93.3 | 7119 | 3 AF329639 | AF329639 Drosophil |
| C 31 | 14 | 93.3 | 21470 | 1 AE008733 | AE008733 Salmone11 |
| C 32 | 14 | 93.3 | 43596 | 9 AC091886 | AC091886 Homo sapi |
| C 33 | 14 | 93.3 | 56883 | 2 AL365182 | AL365182 Human DNA |
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| C 35 | 14 | 93.3 | 119184 | 1 D90909 | D90909 Synchocyst |
| C 36 | 14 | 93.3 | 119638 | 9 AC024575 | AC024575 Homo sapi |
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| C 41 | 14 | 93.3 | 152081 | 9 AC007381 | AC007381 Homo sapi |
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| C 45 | 14 | 93.3 | 169250 | 9 AP002812 | AP002812 Homo sapi |

ALIGNMENTS

RESULT 1
LOCUS AK129669
DEFINITION Homo sapiens cDNA FLJ26158 fis, clone ADG01579.
ACCESSION AK129669
VERSION AK129669.1 GI:34526262
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S.,
Pukuzumi, Y., Fujimori, Y., Komiyama, M., Suzuki, Y., Hata, H.,
Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T.,
Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A.,
Kawakami, B., Nagai, K., Isegai, T. and Sugano, S.
NEDO human cDNA sequencing project

TITLE Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 1924)
AUTHORS Sugano, S. and Suzuki, Y.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail: flicdn@life.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)

COMMENT: NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB; clone selection for
full insert sequencing: RAB and Helix Research Institute.
Location/Qualifiers

FEATURES

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GenCore version 5.1.6
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(without alignment)

8689.645 Million cell updates/sec

Title: US-10-750-965-2

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 2422607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_hcg: *
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5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
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9: gb_pr: *
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11: gb_ats: *
12: gb_gy: *
13: gb_un: *
14: gb_vt: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 718.2 | 60.0 | 6271 | 6 AX718406 | AX718406 Sequence |
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| 5 | 627.4 | 52.4 | 1026 | 1 ECP15A | VO0309 E. coli pla |
| 6 | 627.4 | 52.4 | 2314 | 1 AP432497 | AP432497 Escherich |
| 7 | 627.4 | 52.4 | 2553 | 12 CVE289102 | AJ289102 Cloning v |
| 8 | 627.4 | 52.4 | 2568 | 12 CVE277764 | AJ277764 Cloning v |
| 9 | 627.4 | 52.4 | 3210 | 12 AF361440 | AF361440 Cloning v |
| 10 | 627.4 | 52.4 | 3465 | 6 AX000478 | AX000478 Sequence |
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ALIGNMENTS

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| 27 | 627.4 | 52.4 | 4753 | 12 AP129432 | AP129432 Cloning v |
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| 35 | 627.4 | 52.4 | 6123 | 12 SIN417449 | AJ117449 Shuttle 1 |
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| 38 | 627.4 | 52.4 | 8774 | 12 IVU69267 | IVU69267 Integration |
| 39 | 627.4 | 52.4 | 8774 | 12 AY042185 | AY042185 Reporter |
| 40 | 627.4 | 52.4 | 9065 | 12 AF405698 | AF405698 Reporter |
| 41 | 627.4 | 52.4 | 12168 | 12 AF405696 | AF405696 Reporter |
| 42 | 627.4 | 52.4 | 12248 | 12 AF405697 | AF405697 Reporter |
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| 44 | 627.4 | 52.4 | 18658 | 12 XXU73849 | U73849 Synthetic t |
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| VERSION | AR483258.1 | GI:47245789 | | | |
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| SOURCE | Unknown. | | | | |
| ORGANISM | Unknown. | | | | |
| REFERENCE | Unclassified. | | | | |
| AUTHORS | 1 (bases 1 to 1197) | | | | |
| TITLE | Galen, J.E. | | | | |
| JOURNAL | Plasmid maintenance system for antigen delivery | | | | |
| FEATURES | Patent: US 6703233-A2 09-MAR-2004; | | | | |
| source | Location/Qualifiers | | | | |
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| | Matches 1197; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
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| QY | 121 | ACAAGCATCAAGAAATCTGACGCTCAATCATGCTGCGGAAACCGACAGCATATAA | 180 | | |
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| QY | 241 | TTACCGGTGTCATTCGCTGTTATGCGCGGCTTGTCTCATTCAGCGCTGACATCACT | 300 | | |
| DB | 241 | TTACCGGTGTCATTCGCTGTTATGCGCGGCTTGTCTCATTCAGCGCTGACATCACT | 300 | | |